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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.		
09/530,219	07/27/2000	Christof Niehrs	40168	4031		
75	590 11/28/2001					
Roylance Abra	ams		EXAMI	NER		
Berdo & Goodr	Berdo & Goodman			ANDRES, JANET L		
Suite 600						
1300 19th Stree			ART UNIT	PAPER NUMBER		
Washington, De	C 20036		1646			
			DATE MAILED: 11/28/2001	9		

Please find below and/or attached an Office communication concerning this application or proceeding.



UNITED S DEPARTMENT OF COMMERCE
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SERIAL NUMBER	FILING DATE	FIRST NAMED APPLICANT	ATTORNEY DOCKET NO.
09/530219	07/27/00	Niehrs	40168
03/030213			

EXAMINER			
Janet Andres			
ART UNIT	PAPER NUMBER		
1646	9		

Please find below a communication from the EXAMINER in charge of this application

This application contains sequence disclosures that are encompassed by the definitions for nucleotide and/or amino acid sequences set forth in 37 C.F.R. § 1.821(a)(1) and (a)(2). However, this application fails to comply with the requirements of 37 C.F.R. §§ 1.821-1.825 for the reason(s) set forth on the attached Notice To Comply With Requirements For Patent Applications Containing Nucleotide Sequence And/Or Amino Acid Sequence Disclosures.

APPLICANT IS GIVEN 30 days FROM THE DATE OF THIS LETTER WITHIN WHICH TO COMPLY WITH THE SEQUENCE RULES, 37 C.R.F. §§ 1.821-1.825. Failure to comply with these requirements will result in ABANDONMENT of the application under 37 C.F.R. § 1.821(g). Extensions of time may be obtained by filing a petition accompanied by the extension fee under the provisions of 37 C.F.R. § 1.136. In no case may an applicant extend the period for response beyond the six month statutory period. Direct the response to the undersigned. Applicant is requested to return a copy of the attached Notice to Comply with the response.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Examiner Janet Andres whose telephone number is (703) 305-0557. If the examiner cannot be reached, inquiries can be directed to Supervisory Patent Examiner Yvonne Eyler whose telephone number is (703) 308-6564. The fax number for the organization where this application or proceeding is assigned is (703) 308-4242.

Any inquiry of a general nature or relating to the status of this application should be directed to the Group receptionist whose telephone number is (703) 308-0196.

YVONNE EYLER, PH.D SUPERVISORY PATENT EXAMINER TECHNOLOGY CENTER 1600

Application No.: <u>09/530219</u>

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

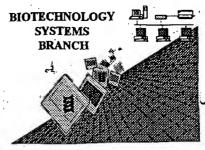
Applicant must file the items indicated below within the time period set the Office action to which the Notice is attached to avoid abandonment under 35 U.S.C. § 133 (extensions of time may be obtained under the provisions of 37 CFR 1.136(a)).

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

X	 This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to the final rulemaking notice published at 55 FR 18230 (May 1, 1990), and 1114 OG 29 (May 15, 1990). If the effective filing date is on or after July 1, 1998, see the final rulemaking notice published at 63 FR 29620 (June 1, 1998) and 1211 OG 82 (June 23, 1998).
	2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
	3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
X	4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
	 The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
	6. The paper copy of the "Sequence Listing" is not the same as the computer readable from of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
	7. Other: Applicant Must Provide:
X	An initial or <u>substitute</u> computer readable form (CRF) copy of the "Sequence Listing".
X	An initial or <u>substitute</u> paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
X	A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).
For	questions regarding compliance to these requirements, please contact:
For	Rules Interpretation, call (703) 308-4216 CRF Submission Help, call (703) 308-4212 tentIn Software Program Support Technical Assistance

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR REPLY

RAW SEQUENCE LISTING ERROR REPORT



NOV 1 3 2001 CIT UENTER 1600/2900

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/530, 2/9ASource: 0/9/530, 2/9/9ADate Processed by STIC: 9/20/200/9

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216. PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax) PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

http://www.uspto.gov/web/offices/pac/checker



NOV 1 3 2001

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION SERIAL NUMBER: 09/530, 2194	
ATTN: NEW RULES CASES	s: Please disregard english "alpha" headers, which were inserted by PTO softv	VARE
1Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3Misaligned Amino Numbering	The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
SVariable Length.	Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6PatentIn 2.0 "bug,"	A "bug" in PatentIn version 2.0 has caused the <220> <223> section to be missing from amino acid sequences(s) Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220> <223> section to the subsequent amino acid sequence. This applies to the mandatory <220> <223> sections for Artificial or Unknown sequences.	
7 Skipped Sequences (OLD RULES)	Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped	
	Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8Skipped Sequences (NEW RULES)	Sequence(s) missing. If Intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11Use of <220>.	Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of Patentln version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	-
13Misuse of n	in can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent	

AMC/MH - Biotechnology Systems Branch - 08/21/2001





OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/530,219A

DATE: 09/20/2001 TIME: 10:43:27

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Does Not Comply Corrected Diskette Needer

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- GLINKA, ANDREI
- 6 <120> TITLE OF INVENTION: AN INHIBITOR PROTEIN OF THE WAT SIGNAL PATH
- 8 <130> FILE REFERENCE: 40168
- 10 <140> CURRENT APPLICATION NUMBER: 09/530,219A
- C--> 11 <141> CURRENT FILING DATE: 2001-09-10
 - 13 <150> PRIOR APPLICATION NUMBER: PCT/DE98/03155
 - 14 <151> PRIOR FILING DATE: 1998-10-27
 - 16 <150> PRIOR APPLICATION NUMBER: DE 197 47 418.7
 - 17 <151> PRIOR FILING DATE: 1997-10-27
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DATE: 09/20/2001

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PATENT APPLICATION: US/09/530,219A

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DATE: 09/20/2001

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RAW SEQUENCE LISTING

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DATE: 09/20/2001 TIME: 10:43:27

Input Set : A:\40168.app

Output Set: N:\CRF3\09202001\I530219A.raw

175 agtocaacac agaaaccaga attggtaata aaactgttca gactcatcaa gaaattgata 360 176 aggttacaga taacagaact ggatcaacaa ttttttccga gacaattatt acatctataa 420 177 agggtggaga aaacaaaaga aatcatgagt gtatcattga tgaagactgt gaaacaggaa 480 178 agtattgcca gttctccacc tttgaataca agtgtcagcc ctgtaaaacc cagcatacac 540 179 actgctcacg agatgttgaa tgctgcggag accagctttg tgtttggggt gagtgcagga 600 180 aagccacttc aagaggagaa aatggtacca tttgtgagaa ccaacatgac tgcaacccag 660 181 gaacgtgctg tgcttttcag aaagaactgc tgtttcctgt gtgcactccg ttacccgaag 720 182 aaggtgaacc ttgccatgat ccttcaaaca gacttctcaa cctgatcacc tgggaactgg 780 183 aacctgatgg agtactagag cgctgcccat gtgcaagtgg cttgatctgc caacctcaga 840 184 gcagccacag tactacatct gtgtgtgaac tgtcctccaa tgaaaccagg aaaaacgaaa 900 185 aagaagatcc cttgaacatg gatgagatgc catttatcag tttaataccc agagatattc 960 186 tttctgatta cgaagaaagc agcgtcattc aggaagtgcg taaagaatta gaaagcctgg 1020 187 aggaccaagc aggtgtgaag totgagcatg accoggotca tgacctattt otgggagatg 1080 188 aaatatgaag ttcaaacacc agtttagtta gtcctagaaa ttgttgtcta gtgtcttgct 1140 189 tacatacacc cttaacagat actgctggat agaagtgcaa taaacatctt cattgagcat 1200 190 ccgttttcgt gcaccaaacc tgcatgttca aattcatgtt gaattcactc aatctttgga 1260 191 ccaaactttc catcaaagac aaatgagaaa ggcatcagtg tttcctttgg attaatcctt 1320 192 tcctttgtac agcagaaata aacgtatcag tactcgtact cattaaaaaa acacacggag 1380 193 cat 196 <210> SEO ID NO: 8 197 <211> LENGTH: 44 198 <212> TYPE: PRT 199 <213> ORGANISM: Artificial Sequence 201 <220> FEATURE: 202 <223> OTHER INFORMATION: Description of Artificial Sequence: Consensus wnt Protein 205 <220> FEATURE: 206 <221> NAME/KEY: MOD_RES 207 <222> LOCATION: (2)..(8) 208 <223> OTHER INFORMATION: Any Amino Acid 210 <220> FEATURE: 211 <221> NAME/KEY: MOD_RES n Eva Summany
Sheet 212 <222> LOCATION: (9) 213 <223> OTHER INFORMATION More Than One Amino Acid 215 <220> FEATURE: 216 <221> NAME/KEY: MOD_RES 217 <222> LOCATION: (10)..(16) 218 <223> OTHER INFORMATION: Any Amino Acid 220 <220> FEATURE: 221 <221> NAME/KEY: MOD_RES 222 <222> LOCATION: (18)..(19) 223 <223> OTHER INFORMATION: Any Amino Acid 225 <220> FEATURE: 226 <221> NAME/KEY: MOD_RES 227 <222> LOCATION: (21)..(26) 228 <223> OTHER INFORMATION: Any Amino Acid 230 <220> FEATURE: 231 <221> NAME/KEY: MOD_RES

232 <222> LOCATION: (28)..(32)





DATE: 09/20/2001

RAW SEQUENCE LISTING PATENT APPLICATION: US/09/530,219A

JS/09/530,219A TIME: 10:43:27

Input Set : A:\40168.app

Output Set: N:\CRF3\09202001\I530219A.raw

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    235 <220> FEATURE:
    236 <221> NAME/KEY: MOD_RES
    237 <222> LOCATION: (35)..(38)
    238 <223> OTHER INFORMATION: Any Amino Acid
    240 <220> FEATURE:
    241 <221> NAME/KEY: MOD_RES
    242 <222> LOCATION: (40)..(41)
    243 <223> OTHER INFORMATION: Any Amino Acid
    245 <220> FEATURE:
    246 <221> NAME/KEY: MOD_RES
    247 <222> LOCATION: (43)
    248 <223> OTHER INFORMATION: Any Amino Acid
    250 <400> SEQUENCE: 8
  252
         1
W--> 254 Cys Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa
    255
                    20
W--> 257 Cys Cys Xaá Xáa Xáa Xaa Cys Xaa Xàa Gly Xaa Cys
    258
                 35
    261 <210> SEQ ID NO: 9
    262 <211> LENGTH: 65
    263 <212> TYPE: PRT
    264 <213> ORGANISM: Artificial Sequence
    266 <220> FEATURE:
    267 <223> OTHER INFORMATION: Description of Artificial Sequence: Consensus wnt
    268
              Protein
    270 <220> FEATURE:
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    272 <222> LOCATION: (2)..(3)
    273 <223> OTHER INFORMATION: Any Amino Acid
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    277 <222> LOCATION: (5)..(6)
    278 <223> OTHER INFORMATION: Any Amino Acid
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    282 <222> LOCATION: (8)..(11)
    283 <223> OTHER INFORMATION: Any Amino Acid
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    287 <222> LOCATION: (14)..(15)
    288 <223> OTHER INFORMATION: Any Amino Acid
    290 <220> FEATURE:
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    292 <222> LOCATION: (17)
    293 <223> OTHER INFORMATION: Any Amino Acid
    295 <220> FEATURE:
    296 <221> NAME/KEY: MOD_RES
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Use of n and/or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to insure a corresponding explanation is presented in the <220> to <223> fields of each sequence using n or Xaa.





VERIFICATION SUMMARY PATENT APPLICATION: US/09/530,219A

DATE: 09/20/2001 19A TIME: 10:43:28

Input Set : A:\40168.app

Output Set: N:\CRF3\09202001\I530219A.raw

 $L:11\ M:271\ C:$ Current Filing Date differs, Replaced Current Filing Date

L:251 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:254 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:257 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:356 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:359 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:362 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:365 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9